
**CERTIFICATE OF MAILING BY "FIRST CLASS MAIL"**

  
Susan B. Lynch

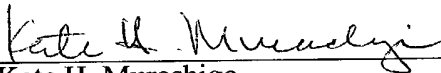
## sd-84170

In the unlikely event that the transmittal letter is separated from this request and the U.S. Patent Office determines that an extension and/or other relief is required, applicants petition for any required relief including extensions of time and authorize the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing to our **Deposit Account No. 03-1952**. However, the Assistant Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

Dated: March 22, 2002

By:

  
Kate H. Murashige  
Registration No. (29,959)

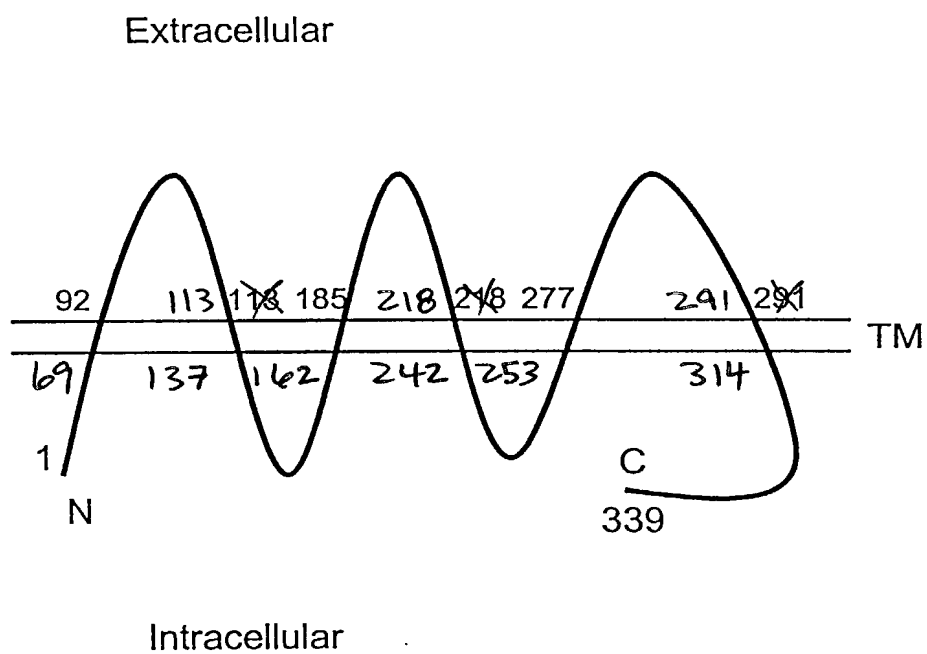
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# FIG. 1A

(SEQ ID NO: 1) 11 20 29 38 47 56  
 5' GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT  
 -----  
 65 74 83 92 101 110  
 ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA  
 -----  
 (SEQ ID NO: 2) M E S R K D I T N Q E E L W K  
 -----  
 119 128 137 146 155 164  
 ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA  
 -----  
 M K P R R N L E E D D Y L H K D T G  
 -----  
 173 182 191 200 209 218  
 GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT  
 -----  
 E T S M L K R P V L L H L H Q T A H  
 -----  
 227 236 245 254 263 272  
 GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA  
 -----  
 A D E F D C P S E L Q H T Q E L F P  
 -----  
 281 290 299 308 317 326  
 CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT  
 -----  
 335 344 353 362 371 380  
 TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT  
 -----  
 X T L L R E V I H P L A T S H Q Q Y  
 -----  
 389 398 407 416 425 434  
 TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC  
 -----  
 F Y K I P I L V I N K V L P M V S I  
 -----  
 443 452 461 470 479 488  
 ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT  
 -----  
 T L L A L V Y L P G V I A A I V Q L  
 -----  
 497 506 515 524 533 542  
 CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA  
 -----  
 H N G T K Y K K F P H W L D K W M L  
 -----  
 551 560 569 578 587 596  
 ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT  
 -----  
 T R K Q F G L L S F F F A V L H A I  
 -----  
 605 614 623 632 641 650  
 TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG  
 -----  
 Y S L S Y P M R R S Y R Y K L L N W  
 -----

**K**

**FIG. 1B**



## FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG  
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT  
AAC AGC AAG 3' (SEQ ID NO: 3)

**FIG. 4-1**

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC  
ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG  
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC  
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACA  
GTGGCACTTGCCAATTAATAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT  
CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG  
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATGTCCAACCTTCATAATGGAACCAA  
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT  
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT  
ATCAACAGGTCCAACAAAATAAAGAAGATGCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT  
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG  
AGAGAAATTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT  
ATAGAATATGTTGACTTTACCCATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCGAATT  
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTCCTAGACATAAATAAAAGGCAT  
TAAATATTTCTTTGTTTTTTTTTTTTGTTTGTGTTGTTTTGTTTGTGTTGTTTTGTTTGTGTTTTTTGAGATGAAGTCTCG  
CTCTGTGCCCATGCTGGAGTACAGTGGCAGCATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTCT  
TCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTAGTA  
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC  
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT  
GCTACCCATCTAATGTGATATTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAATATTCTTTTACC  
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTTAGCACTTTCAGAAACAAAACTCTCTCCTTGAAA  
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT  
ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT  
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGCTGACAAAGATTCAAAGGACTAAA  
TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT  
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGAAAGTATGC  
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCAGAGAATTTCTTAATTTTGTTAGGTTTCTAG  
CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA  
TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTACTATATGTAC

FIG. 4-2

1703-011.PC FIG. 4 - SHEET 2 OF 2

ATACCTAGCCCATAGGTATACAATACACATTTGGTAAACTAATTTTCAACCAATGACATGTATTTTCAACT  
AGTAACCTAGAAATGTTTCACTTAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA  
ACGCAAACCTAGCTATTTGATTGTATTCACCTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT  
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT  
TGAGATTACATAGGTGAACAACTATTTTAAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA  
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC  
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACCTTCATTATTCATTTATCAAAATCAGAGTGAATCA  
CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT  
TTAATTGAGAATCTAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT  
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAG  
GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG  
TTCACCTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAGAGCAGAAAGATG  
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG  
ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTTCTTTTGCAGAGCAAGCTAGGA  
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG  
TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGTCTGATATTTAAAGCATACTATT  
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACCTGAG  
ATATGTTCCCAGTTGTAGAACTACTGTTTACACACATTTTGTTCATATTGATATATTTTATCACCAACATTTCA  
AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:6)



FIG. 5

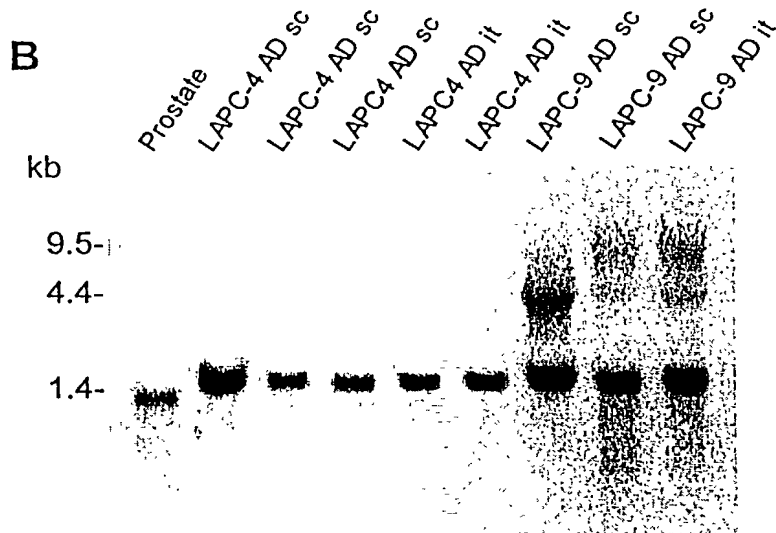
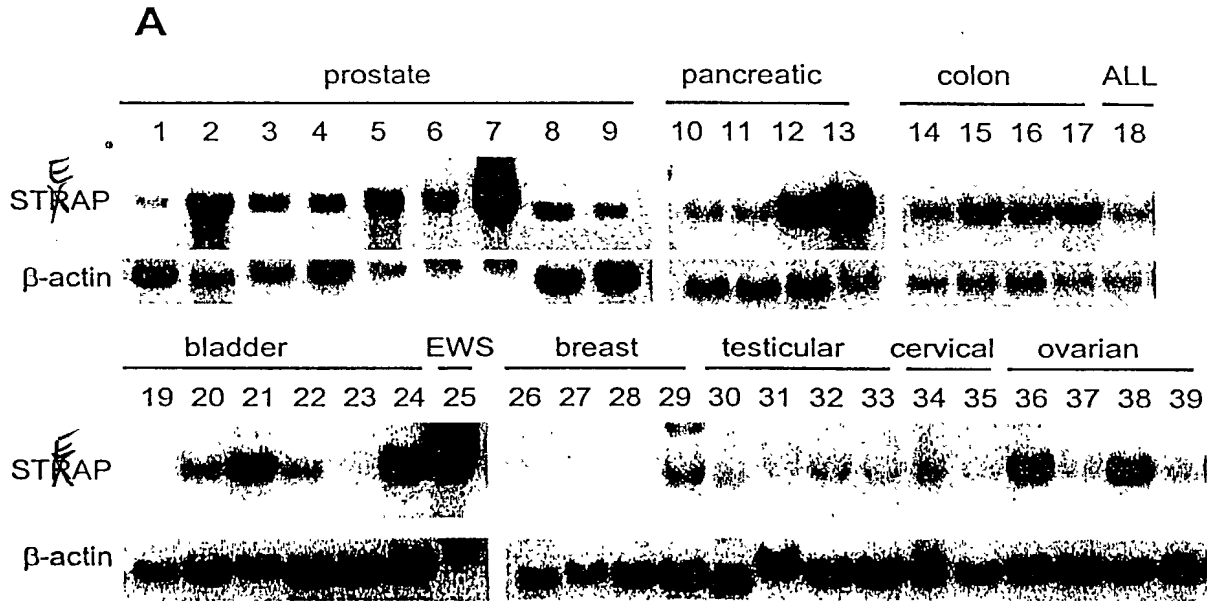
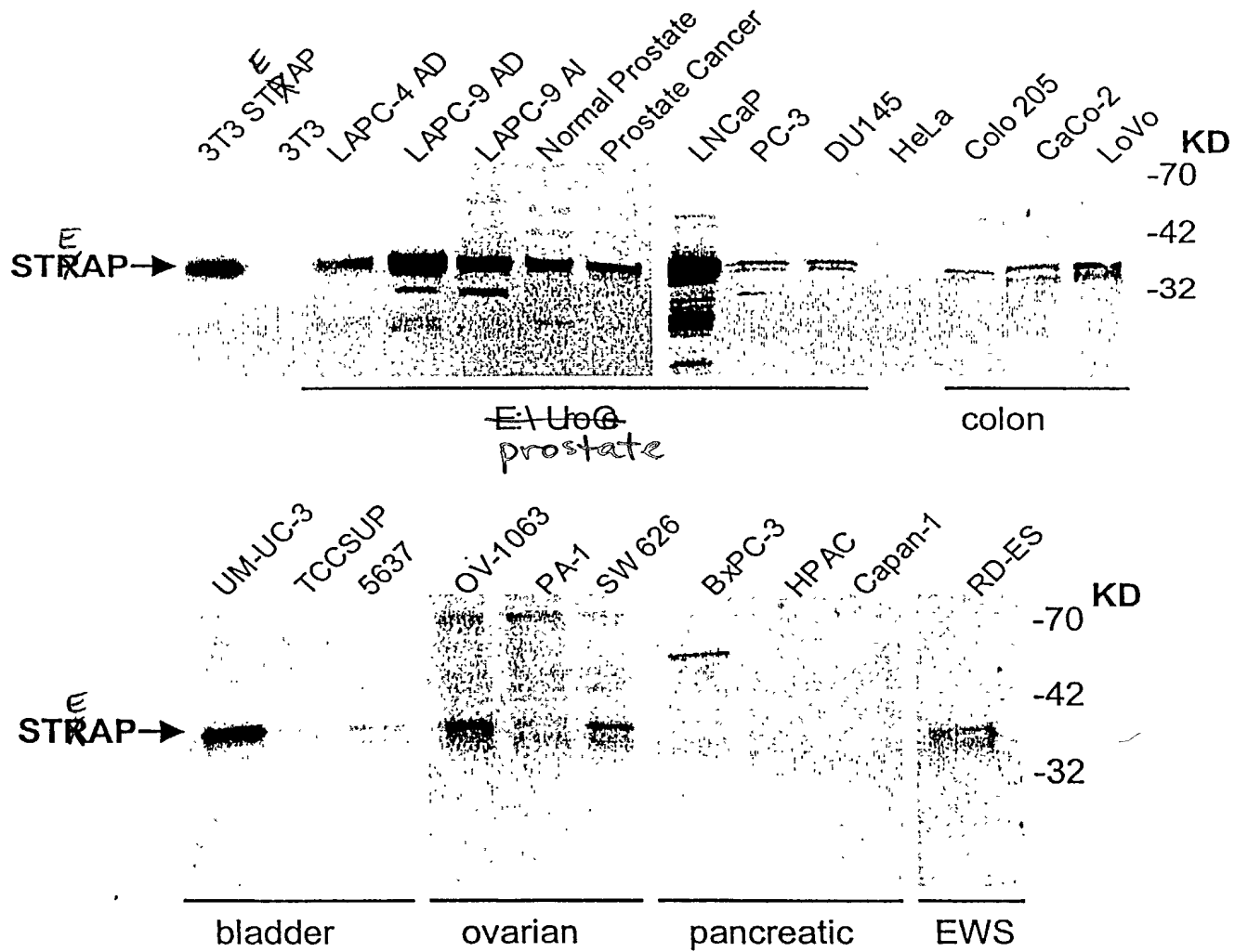


FIG. 6





# FIG. 9

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5'   10      19      28      37      46      55
    GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT ATA GTT GCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile Val Ala

      64      73      82      91      100      109
    ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA GGT CTT CTG GCA GCT GCT TAT CAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala Ala Ala Tyr Gln

      118      127      136      145      154      163
    CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA ACC TGG TTA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu

      172      181      190      199      208      217
    CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG GTC CAT GTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val

      226      235      244      253      262      271
    GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG TTT CTC AAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn

      280      289      298      307      316      325
    ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT GAG GAA GAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu

      334      343      352      361      370      379
    GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT GGC TTA CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu

      388      397      406      415      424      433
    TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA AAC TGG AGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg

      442      451      460      469      478      487
    GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC ATA AGT ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile Ser Thr

      496      505      514
    TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT 3' (SEQ ID NO: 7)
    --- --- --- --- --- --- --- --- --- --- --- ---
    Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala (SEQ ID NO: 8)

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R80991 (placental EST)  
ggccgcggcancgccctacgacatgggtcaacctggcagtcgaagcaggtctctggccanacaagagccacctctggggtg  
aaggaggagggtctggcggatggagatctacctctccctgggagtgctggccctcggcacgttgctccctgctggccg  
tgacctcactgcccgtccattgcaaactcgctcaactggaggaggagttcagcttcggttcagtcctcactgggctttgt  
ggccntcggtgctgagcacactnccacgctcaacctacggctggaccgcgccttcgaggagagccgctacaagttc  
tacctnccctcccaccttcacgntcacgctctgggtgcacctcgcttcggttcacctctgggccaaagccctgtttntac  
tgacctgcattcagccgnaga (SEQ ID NO: 12)

# FIG. 11A

STRAP-1	106	FYKIPILVINKVLPVMSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFG
STRAP-2	2	FYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTYRRFPFWLETWLQCRKQLG
		***** *
STRAP-1	166	LLSFFFVAVLHAIYSLSPMRRSYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIV
STRAP-2	62	LLSFFFAMVHVAYSCLPMRRSERYLFNLMAYQQVHANIENSWNEEEVWRIEMYISFGIM
		***** *
STRAP-1	226	GLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWN <sup>6</sup>
STRAP-2	122	SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR
		* *

(Portion of SEQ ID: 2)

(Portion of SEQ ID: 8)

# FIG. 11B

STRAP-1 STRAP-2 STRAP-3 STRAP-4	1	15 16	30 31	45 46	60 61	75 76	90
		MESRDIITNOEELWK	MKPRRNLEEDDYHLK	DTGETSMKRVPVLH	LHQTADADEFDCPSE	LQHTQELFPQWHLPI	KIAAIIASLTFLYTL
		-----	-----	-----	-----	-----	-----
		-----	-----	-----	-----	-----	-----
STRAP-1 STRAP-2 STRAP-3 STRAP-4	91	105 106	120 121	135 136	150 151	165 166	180
		LREVIHPLATSHQOY	FYKIPILVINKVLPFM	VSITLLALVILPGVI	AAIVQLHNGTKYKKE	PHWLDKWMMLTRKQFG	LLSFFFAVLHAIYSL
		-----	-----	-----	-----	-----	-----
		-----	-----	-----	-----	-----	-----
STRAP-1 STRAP-2 STRAP-3 STRAP-4	181	195 196	210 211	225 226	240 241	255 256	270
		SYPHRSYRYKILNM	AYQOVQONKEDAWIE	HDVWRMEIYVSLGIV	GLAILADLAVTSIPS	VSPSLTWREFHYIQS	KLGIIVSLDGTIHAL
		CLPFRSERYLFLNM	AYQOVHANIEANSWE	BEVWRIEMYLISFGIM	SIGLLSILLAVTSIPS	VSNALNNREFSFQIS	TLGYVALLISTFHVQ
		-----	-----	-----	-----	-----	-----
STRAP-1 STRAP-2 STRAP-3 STRAP-4	271	285 286	300 301	315 316	330 331	345 346	360
		IFAWNKWIDIKQFVW	YTPPTFMIAVFLPIV	VLIFKSLFLFCGRK	KILKIRHGWEDVTKI	NKTEICSQL	339 (SEQ ID NO: 2)
		-----	-----	-----	-----	-----	-----
		-----	-----	-----	-----	-----	-----

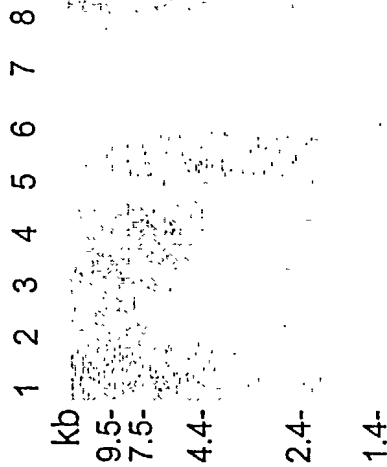
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1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus



# FIG. 15

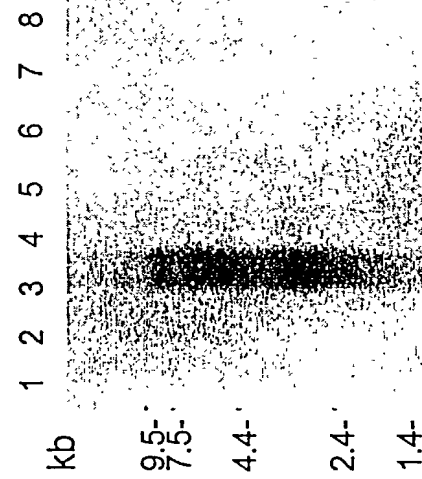
FIG. 15A



A

1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas

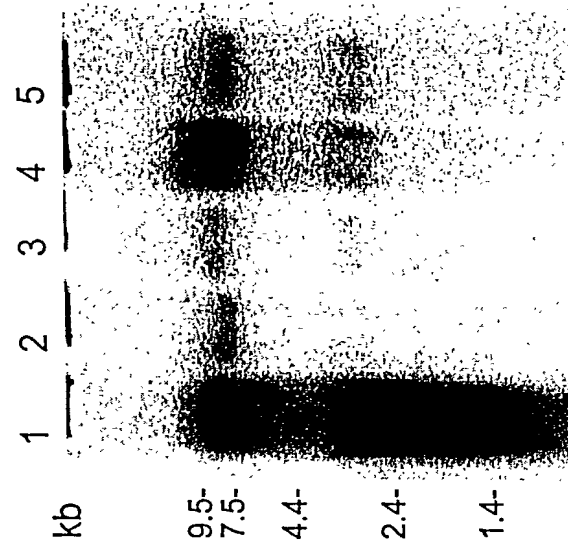
FIG. 15B



B

1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Ovary
6. Small Intestine
7. Colon
8. Leukocytes

FIG. 15C



C

1. Prostate
2. LAPC-4 AD
3. LAPC-4 AI
4. LAPC-9 AD
5. LAPC-9 AI

**FIG. 17**

**GDB Compreher**

